

10/576030

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1

SEQUENCE LISTING

<110> Hokko CHEMICAL INDUSTRY CO., LTD.

<120> METHOD FOR PRODUCING SCYLLO-INOSITOL

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<150> JP2003-353490

<151> 2003-10-14

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<150> JP2004-18128

<151> 2004-1-27

<150> JP2004-194088

<151> 2004-6-30

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<170> PatentIn version 3.1

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Met Val Gly Gly Gln Gly Ala Phe Ile Gly Ala Val His Arg Ile
      20          25          30
gcg gcc cgg ctg gat gac cgt tac gag ctg gtg gcc gga gcg ctt tcc      144
Ala Ala Arg Leu Asp Asp Arg Tyr Glu Leu Val Ala Gly Ala Leu Ser
      35          40          45
tcc gat ccc gcg cgt gcc gcc gcc tcg gca aca ctg ctc ggc att gcg      192
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      50          55          60
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Pro Glu Arg Ser Tyr Ala Ser Phe Glu Asp Met Ala Ala Thr Glu Ala
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ggc cgg gag gat ggc atc gag gca gtc gcc atc gtc acc ccc aac cat      288
Gly Arg Glu Asp Gly Ile Glu Ala Val Ala Ile Val Thr Pro Asn His
      85          90          95
ctg cat ttt gcc ccg tcc aag gcc ttt ctc gaa gcc ggc atc cac gtc      336
Leu His Phe Ala Pro Ser Lys Ala Phe Leu Glu Ala Gly Ile His Val
      100         105         110
atc tgc gac aag ccg gtg acc gcg acg ctg gaa gaa gcg aag gca ctg      384
Ile Cys Asp Lys Pro Val Thr Ala Thr Leu Glu Glu Ala Lys Ala Leu
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His Asn Tyr Thr Gly Tyr Pro Met Val Arg His Ala Arg Glu Leu Val  
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Arg Leu Asp Asp Asn Ala His Val Met Met Arg Phe Lys Pro Lys Gly  
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Gly Lys Gln Pro Ala Arg Gly Met Leu Trp Cys Ser Gln Val Ala Val  
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Gly His Glu Asn Gly Leu Lys Ile Arg Leu Tyr Gly Asp Lys Ala Gly  
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 Leu Glu Glu Ile Thr Asn Asp Pro Ala Ile Glu Leu Val Ile Val Thr  
 65 70 75 80  
 acc ccg agc ggc ctt cat tac gag cat act atg gca tgc ata cag gcc 288  
 Thr Pro Ser Gly Leu His Tyr Glu His Thr Met Ala Cys Ile Gln Ala  
 85 90 95  
 gga aaa cat gtt gtg atg gaa aaa cca atg aca gca acg gcc gaa gag 336  
 Gly Lys His Val Val Met Glu Lys Pro Met Thr Ala Thr Ala Glu Glu  
 100 105 110

ggg gaa aca tta aaa agg gct gcc gat gaa aaa ggc gta tta tta agc Gly Glu Thr Leu Lys Arg Ala Ala Asp Glu Lys Gly Val Leu Leu Ser 115 120 125	384
gta tat cat aac cga cgc tgg gat aac gat ttt tta acg att aaa aag Val Tyr His Asn Arg Arg Trp Asp Asn Asp Phe Leu Thr Ile Lys Lys 130 135 140	432
ctg atc tct gag gga tcc ctt gaa gat atc aat aca tat caa gtt tcc Leu Ile Ser Glu Gly Ser Leu Glu Asp Ile Asn Thr Tyr Gln Val Ser 145 150 155 160	480
tat aac cgc tac aga cct gaa gtt caa gcg cgg tgg cgg gaa aaa gaa Tyr Asn Arg Tyr Arg Pro Glu Val Gln Ala Arg Trp Arg Glu Lys Glu 165 170 175	528
ggc act gcc act ggt acg ctg tat gat ctc ggc tcc cac atc ata gac Gly Thr Ala Thr Gly Thr Leu Tyr Asp Leu Gly Ser His Ile Ile Asp 180 185 190	576
caa acc ctg cat ttg ttt ggg atg cct aaa gcc gtg act gca aac gtg Gln Thr Leu His Leu Phe Gly Met Pro Lys Ala Val Thr Ala Asn Val 195 200 205	624
atg gcc cag cgg gaa aat gcc gaa acg gtt gac tat ttt cat tta acc Met Ala Gln Arg Glu Asn Ala Glu Thr Val Asp Tyr Phe His Leu Thr 210 215 220	672
ctg gat tat ggc aag ctt caa gcc att cta tac gga gga tca atc gtt Leu Asp Tyr Gly Lys Leu Gln Ala Ile Leu Tyr Gly Gly Ser Ile Val 225 230 235 240	720
cgc gca aac gga cct cgt tat caa atc cat gga aaa gat tct agc ttt Pro Ala Asn Gly Pro Arg Tyr Gln Ile His Gly Lys Asp Ser Ser Phe 245 250 255	768
atc aaa tat gga att gac gga cag gaa gac gca ctc aga gcg gga aga Ile Lys Tyr Gly Ile Asp Gly Gln Glu Asp Ala Leu Arg Ala Gly Arg 260 265 270	816
aaa cca gag gat gac agc tgg ggt gcg gat gtt ccg gag ttt tac gga Lys Pro Glu Asp Asp Ser Trp Gly Ala Asp Val Pro Glu Phe Tyr Gly 275 280 285	864
aag ctt aca acc att cgt ggc tcc gac aaa aaa aca gaa acg att cca Lys Leu Thr Thr Ile Arg Gly Ser Asp Lys Lys Thr Glu Thr Ile Pro 290 295 300	912
tca gta aat ggc tcc tac ctt act tat tac cgt aaa ata gcg gaa agc Ser Val Asn Gly Ser Tyr Leu Thr Tyr Tyr Arg Lys Ile Ala Glu Ser 305 310 315 320	960
ata cga gaa ggt gct gcg ctg cca gtc act gct gag gaa ggt att aat Ile Arg Glu Gly Ala Ala Leu Pro Val Thr Ala Glu Glu Gly Ile Asn 325 330 335	1008
gtc atc cgc atc att gaa gcc gcg atg gaa agc agt aaa gag aaa cga Val Ile Arg Ile Ile Glu Ala Ala Met Glu Ser Ser Lys Glu Lys Arg 340 345 350	1056
acc att atg ctg gag cac taa Thr Ile Met Leu Glu His 355	1077

<210> 8  
 <211> 358  
 <212> PRT  
 <213> *Bacillus subtilis*

<400> 8

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Gly Ile Leu Gly Tyr Gly Leu Ser Gly Ser Val Phe His Gly Pro Leu
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Leu Asp Val Leu Asp Glu Tyr Gln Ile Ser Lys Ile Met Thr Ser Arg
          35           40           45
Thr Glu Glu Val Lys Arg Asp Phe Pro Asp Ala Glu Val Val His Glu
          50           55           60
Leu Glu Glu Ile Thr Asn Asp Pro Ala Ile Glu Leu Val Ile Val Thr
65           70           75           80
Thr Pro Ser Gly Leu His Tyr Glu His Thr Met Ala Cys Ile Gln Ala
          85           90           95
Gly Lys His Val Val Met Glu Lys Pro Met Thr Ala Thr Ala Glu Glu
          100          105          110
Gly Glu Thr Leu Lys Arg Ala Ala Asp Glu Lys Gly Val Leu Leu Ser
          115          120          125
Val Tyr His Asn Arg Arg Trp Asp Asn Asp Phe Leu Thr Ile Lys Lys
          130          135          140
Leu Ile Ser Glu Gly Ser Leu Glu Asp Ile Asn Thr Tyr Gln Val Ser
145          150          155          160
Tyr Asn Arg Tyr Arg Pro Glu Val Gln Ala Arg Trp Arg Glu Lys Glu
          165          170          175
Gly Thr Ala Thr Gly Thr Leu Tyr Asp Leu Gly Ser His Ile Ile Asp
          180          185          190
Gln Thr Leu His Leu Phe Gly Met Pro Lys Ala Val Thr Ala Asn Val
          195          200          205
Met Ala Gln Arg Glu Asn Ala Glu Thr Val Asp Tyr Phe His Leu Thr
          210          215          220
Leu Asp Tyr Gly Lys Leu Gln Ala Ile Leu Tyr Gly Gly Ser Ile Val
225          230          235          240
Pro Ala Asn Gly Pro Arg Tyr Gln Ile His Gly Lys Asp Ser Ser Phe
          245          250          255
Ile Lys Tyr Gly Ile Asp Gly Gln Glu Asp Ala Leu Arg Ala Gly Arg
          260          265          270
Lys Pro Glu Asp Asp Ser Trp Gly Ala Asp Val Pro Glu Phe Tyr Gly
          275          280          285
Lys Leu Thr Thr Ile Arg Gly Ser Asp Lys Lys Thr Glu Thr Ile Pro
          290          295          300
Ser Val Asn Gly Ser Tyr Leu Thr Tyr Tyr Arg Lys Ile Ala Glu Ser
305          310          315          320

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Ile Arg Glu Gly Ala Ala Leu Pro Val Thr Ala Glu Glu Gly Ile Asn  
 325 330 335  
 Val Ile Arg Ile Ile Glu Ala Ala Met Glu Ser Ser Lys Glu Lys Arg  
 340 345 350  
 Thr Ile Met Leu Glu His  
 355

<210> 9  
 <211> 1170  
 <212> DNA  
 <213> Agrobacterium sp.

<220>  
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 <222> (1).. (1170)  
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 atg gtc ggc ggc ggt cag ggc gcc ttt atc ggt gcg gtg cac cgc ata 96  
 Met Val Gly Gly Gly Gln Gly Ala Phe Ile Gly Ala Val His Arg Ile  
 20 25 30  
 gcg gcc cgg ctg gat gac cgt tac gag ctc gtg gcc gga gcg ctt tcc 144  
 Ala Ala Arg Leu Asp Asp Arg Tyr Glu Leu Val Ala Gly Ala Leu Ser  
 35 40 45  
 tcc gat ccc gcg cgt gcg gcc gct tcg gca acc ctg ctc gcc atc gcg 192  
 Ser Asp Pro Ala Arg Ala Ala Ser Ala Thr Leu Leu Gly Ile Ala  
 50 55 60  
 ccg gag cgt tcc tat gcc tca ttc gag gag atg gct gcg gca gag gcc 240  
 Pro Glu Arg Ser Tyr Ala Ser Phe Glu Glu Met Ala Ala Ala Glu Ala  
 65 70 75 80  
 ggt cga gac gac ggt atc gag gca gtc gcc atc gtg acg ccc aat cac 288  
 Gly Arg Asp Asp Gly Ile Glu Ala Val Ala Ile Val Thr Pro Asn His  
 85 90 95  
 ctc cat ttt gcg ccc tca aag gcc ttt ctc gag gcc ggt att cac gtc 336  
 Leu His Phe Ala Pro Ser Lys Ala Phe Leu Glu Ala Gly Ile His Val  
 100 105 110  
 atc tgc gac aag cct gtg acc gcg aca ctt gag gaa gca aag gcg ctg 384  
 Ile Cys Asp Lys Pro Val Thr Ala Thr Leu Glu Glu Ala Lys Ala Leu  
 115 120 125  
 gcc gag atc gtc agg gcg tcg gac agc ctg ttt gtc ctg acg cat aat 432  
 Ala Glu Ile Val Arg Ala Ser Asp Ser Leu Phe Val Leu Thr His Asn  
 130 135 140  
 tac acc ggc tac gcc atg ctg cgg cag atg cgg cag atg gtg gct gat 480  
 Tyr Thr Gly Tyr Ala Met Leu Arg Gln Met Arg Gln Met Val Ala Asp

145	150	155	160	
gga gcc att ggc aag ctg cgc cac gtt cag gcc gaa tat gcc cag gac				528
Gly Ala Ile Gly Lys Leu Arg His Val Gln Ala Glu Tyr Ala Gln Asp				
	165	170	175	
tgg ctg acc gag gcg gtt gag aag acc ggt gcg aag ggg gcg gaa tgg				576
Trp Leu Thr Glu Ala Val Glu Lys Thr Gly Ala Lys Gly Ala Glu Trp				
	180	185	190	
cgc acc gat ccc agc cgc tcc ggc gcg ggc gcc atc ggc gat atc				624
Arg Thr Asp Pro Ser Arg Ser Gly Ala Gly Gly Ala Ile Gly Asp Ile				
	195	200	205	
ggc acc cac gcc ttc aac gct gcc gcc ttc gtt acc ggt gaa atc ccg				672
Gly Thr His Ala Phe Asn Ala Ala Ala Phe Val Thr Gly Glu Ile Pro				
	210	215	220	
aag agt ctt tat gcc gac ctg acc tct ttc gtg ccg ggc cgg cag ctg				720
Lys Ser Leu Tyr Ala Asp Leu Thr Ser Phe Val Pro Gly Arg Gln Leu				
	225	230	235	240
gat gac agc gcc aat att ctt ttg cgt tac gaa agc ggc gcc aag ggc				768
Asp Asp Ser Ala Asn Ile Leu Leu Arg Tyr Glu Ser Gly Ala Lys Gly				
	245	250	255	
atg ctt tgg gca agc cag atc gca gtc ggc aat gaa aac gcg ctg tcg				816
Met Leu Trp Ala Ser Gln Ile Ala Val Gly Asn Glu Asn Ala Leu Ser				
	260	265	270	
ctg cgg gtc tac ggc gaa aag ggc ggg ctt gaa tgg cac cac gcg gtg				864
Leu Arg Val Tyr Gly Glu Lys Gly Gly Leu Glu Trp His His Arg Val				
	275	280	285	
ccg gat gag ctg tgg ttc acc cct tac ggc gag ccg aag cgg ctc ata				912
Pro Asp Glu Leu Trp Phe Thr Pro Tyr Gly Glu Pro Lys Arg Leu Ile				
	290	295	300	
acc cgc aac ggc gca ggc gca gga gcc gcg gcc aac cgt gtc agc cgc				960
Thr Arg Asn Gly Ala Gly Ala Gly Ala Ala Ala Asn Arg Val Ser Arg				
	305	310	315	320
gtg cca tcg ggg cac ccg gaa gga tac ctc gag ggt ttc gcg acg atc				1008
Val Pro Ser Gly His Pro Glu Gly Tyr Leu Glu Gly Phe Ala Thr Ile				
	325	330	335	
tac cgc gaa gcc gca gat gca atc att gcc aaa agg gag gga aaa gca				1056
Tyr Arg Glu Ala Ala Asp Ala Ile Ile Ala Lys Arg Glu Gly Lys Ala				
	340	345	350	
gcc gcc ggg gag gtg att tac ccc ggc atg gag gac ggc ctt gcg ggt				1104
Ala Ala Gly Glu Val Ile Tyr Pro Gly Met Glu Asp Gly Leu Ala Gly				
	355	360	365	
ctc gca ttc atc gat gcc gcc gtt cgc tcc agc cag acc tcg acc tgg				1152
Leu Ala Phe Ile Asp Ala Ala Val Arg Ser Ser Gln Thr Ser Thr Trp				
	370	375	380	
atc aat atc gat atc tag				1170
Ile Asn Ile Asp Ile				
385				

<210> 10  
 <211> 389  
 <212> PRT  
 <213> Agrobacterium sp.

<400> 10

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Met Ser Ser Ala Pro Lys Lys Phe Asp Ser Arg Arg Ile Arg Leu Gly
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20      25      30
Ala Ala Arg Leu Asp Asp Arg Tyr Glu Leu Val Ala Gly Ala Leu Ser
35      40      45
Ser Asp Pro Ala Arg Ala Ala Ser Ala Thr Leu Leu Gly Ile Ala
50      55      60
Pro Glu Arg Ser Tyr Ala Ser Phe Glu Glu Met Ala Ala Ala Glu Ala
65      70      75      80
Gly Arg Asp Asp Gly Ile Glu Ala Val Ala Ile Val Thr Pro Asn His
85      90      95
Leu His Phe Ala Pro Ser Lys Ala Phe Leu Glu Ala Gly Ile His Val
100     105     110
Ile Cys Asp Lys Pro Val Thr Ala Thr Leu Glu Glu Ala Lys Ala Leu
115     120     125
Ala Glu Ile Val Arg Ala Ser Asp Ser Leu Phe Val Leu Thr His Asn
130     135     140
Tyr Thr Gly Tyr Ala Met Leu Arg Gln Met Arg Gln Met Val Ala Asp
145     150     155     160
Gly Ala Ile Gly Lys Leu Arg His Val Gln Ala Glu Tyr Ala Gln Asp
165     170     175
Trp Leu Thr Glu Ala Val Glu Lys Thr Gly Ala Lys Gly Ala Glu Trp
180     185     190
Arg Thr Asp Pro Ser Arg Ser Gly Ala Gly Gly Ala Ile Gly Asp Ile
195     200     205
Gly Thr His Ala Phe Asn Ala Ala Ala Phe Val Thr Gly Glu Ile Pro
210     215     220
Lys Ser Leu Tyr Ala Asp Leu Thr Ser Phe Val Pro Gly Arg Gln Leu
225     230     235     240
Asp Asp Ser Ala Asn Ile Leu Leu Arg Tyr Glu Ser Gly Ala Lys Gly
245     250     255
Met Leu Trp Ala Ser Gln Ile Ala Val Gly Asn Glu Asn Ala Leu Ser
260     265     270
Leu Arg Val Tyr Gly Glu Lys Gly Gly Leu Glu Trp His His Arg Val
275     280     285
Pro Asp Glu Leu Trp Phe Thr Pro Tyr Gly Glu Pro Lys Arg Leu Ile
290     295     300
Thr Arg Asn Gly Ala Gly Ala Gly Ala Ala Ala Asn Arg Val Ser Arg
305     310     315     320
Val Pro Ser Gly His Pro Glu Gly Tyr Leu Glu Gly Phe Ala Thr Ile
325     330     335

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Tyr Arg Glu Ala Ala Asp Ala Ile Ile Ala Lys Arg Glu Gly Lys Ala  
                   340                  345                  350  
 Ala Ala Gly Glu Val Ile Tyr Pro Gly Met Glu Asp Gly Leu Ala Gly  
                   355                  360                  365  
 Leu Ala Phe Ile Asp Ala Ala Val Arg Ser Ser Gln Thr Ser Thr Trp  
                   370                  375                  380  
 Ile Asn Ile Asp Ile  
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<210> 11  
 <211> 1188  
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 <213> *Agrobacterium* sp.

<220>  
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 <222> (1).. (1188)  
 <223>

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 ctc ggc atg gtg ggc ggt ggt tct ggt gcc ttt atc ggt ggt gtt cac 96  
 Leu Gly Met Val Gly Gly Gly Ser Gly Ala Phe Ile Gly Gly Val His  
                   20                  25                  30  
 cgc atg gcg gcg cgg ctc gac aat cgt ttc gat ctc gtg gca ggg gcg 144  
 Arg Met Ala Ala Arg Leu Asp Asn Arg Phe Asp Leu Val Ala Gly Ala  
                   35                  40                  45  
 ctg tct tcg acc ccg gaa aaa tcc ctc gcc tcc ggc cgt gaa ctg ggg 192  
 Leu Ser Ser Thr Pro Glu Lys Ser Leu Ala Ser Gly Arg Glu Leu Gly  
                   50                  55                  60  
 ctc gat ccc gag cgt tgc tac ggc tcg ttc gag gag atg gcc gaa aag 240  
 Leu Asp Pro Glu Arg Cys Tyr Gly Ser Phe Glu Glu Met Ala Glu Lys  
   65                  70                  75                  80  
 gag gcg cta cgc gag gat ggc ata gag gcg gtg gcg atc gtc acg ccc 288  
 Glu Ala Leu Arg Glu Asp Gly Ile Glu Ala Val Ala Ile Val Thr Pro  
                   85                  90                  95  
 aac cac gtg cat tat ccg gcg gcg aag gcg ttt ctg gag cgt ggc atc 336  
 Asn His Val His Tyr Pro Ala Ala Lys Ala Phe Leu Glu Arg Gly Ile  
                   100                  105                  110  
 cat gtc atc tgc gac aag ccg ctg acc tcc aat ctg gaa gac gcg aag 384  
 His Val Ile Cys Asp Lys Pro Leu Thr Ser Asn Leu Glu Asp Ala Lys  
                   115                  120                  125  
 aag ctg aag gac gtc gcc gac aag gcc gat gcg ctg ttc atc ctg acg 432  
 Lys Leu Lys Asp Val Ala Asp Lys Ala Asp Ala Leu Phe Ile Leu Thr  
   130                  135                  140



cat aat tac acc ggc tat ccg atg gtg cgg cat gca cgg gaa ctg gtg	480
His Asn Tyr Thr Gly Tyr Pro Met Val Arg His Ala Arg Glu Leu Val	
145 150 155 160	
gaa tcg ggc gct ctc ggc acg atc cgt ctg gtg cag atg gag tat ccg	528
Glu Ser Gly Ala Leu Gly Thr Ile Arg Leu Val Gln Met Glu Tyr Pro	
165 170 175	
cag gac tgg ctg gcg gaa ccc atc gag cag acg ggc gcc aaa cag gct	576
Gln Asp Trp Leu Ala Glu Pro Ile Glu Gln Thr Gly Ala Lys Gln Ala	
180 185 190	
gtc tgg cgc acc gac ccg gcc caa tcc ggt gcg ggt ggt tcc aca ggc	624
Val Trp Arg Thr Asp Pro Ala Gln Ser Gly Ala Gly Gly Ser Thr Gly	
195 200 205	
gat atc ggc acg cat gcc tat aat ctc ggc tgc ttc att tcc ggt ctg	672
Asp Ile Gly Thr His Ala Tyr Asn Leu Gly Cys Phe Ile Ser Gly Leu	
210 215 220	
gaa gtc gac gaa ctg gcg gca gat gtg cat acc ttt gtc gaa ggc cgc	720
Glu Val Asp Glu Leu Ala Ala Asp Val His Thr Phe Val Glu Gly Arg	
225 230 235 240	
cgg ctg gac gac aat gcg cat gtg atg ctg cgt ttc aag ccg aag ggt	768
Arg Leu Asp Asp Asn Ala His Val Met Leu Arg Phe Lys Pro Lys Gly	
245 250 255	
ggc aag cag ccg gca aag ggg ctg ctc tgg tgc agc cag gtt gcg gtc	816
Gly Lys Gln Pro Ala Lys Gly Leu Leu Trp Cys Ser Gln Val Ala Val	
260 265 270	
ggc cac gaa aac ggc ctg aaa gtt cgt gtg tat ggt gac aag gcc ggc	864
Gly His Glu Asn Gly Leu Lys Val Arg Val Tyr Gly Asp Lys Ala Gly	
275 280 285	
atc gaa tgg acg cag gcc gac ccg aac tat ctc tgg ttc acg aag ctt	912
Ile Glu Trp Thr Gln Ala Asp Pro Asn Tyr Leu Trp Phe Thr Lys Leu	
290 295 300	
ggc gag ctg aag cag ttg atc acc cgc ggc ggt gcc ggg gca ggg gct	960
Gly Glu Leu Lys Gln Leu Ile Thr Arg Gly Gly Ala Gly Ala Gly Ala	
305 310 315 320	
gcc gca gca cgc gtc acc cgc atc cct tcc ggc cac ccg gaa ggt tat	1008
Ala Ala Ala Arg Val Thr Arg Ile Pro Ser Gly His Pro Glu Gly Tyr	
325 330 335	
ctc gaa gcc ttc gca acg atc tat acc gag gcg gcg cat gcc atc gaa	1056
Leu Glu Ala Phe Ala Thr Ile Tyr Thr Glu Ala Ala His Ala Ile Glu	
340 345 350	
gcc cgc cgc acc ggc tcg gtg ctc gac aag gcc gtg att tac ccg acc	1104
Ala Arg Arg Thr Gly Ser Val Leu Asp Lys Ala Val Ile Tyr Pro Thr	
355 360 365	
gtc gat gat ggc gta aag ggt gtc gcc ttt gtt acg gcc tgc atc gag	1152
Val Asp Asp Gly Val Lys Gly Val Ala Phe Val Thr Ala Cys Ile Glu	
370 375 380	
tcc ggc aag aag aac ggt gtc tgg gtg aag ctg taa	1188
Ser Gly Lys Lys Asn Gly Val Trp Val Lys Leu	
385 390 395	

<210> 12  
 <211> 395  
 <212> PRT  
 <213> *Agrobacterium* sp.

<400> 12

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Arg Met Ala Ala Arg Leu Asp Asn Arg Phe Asp Leu Val Ala Gly Ala
35      40      45
Leu Ser Ser Thr Pro Glu Lys Ser Leu Ala Ser Gly Arg Glu Leu Gly
50      55      60
Leu Asp Pro Glu Arg Cys Tyr Gly Ser Phe Glu Glu Met Ala Glu Lys
65      70      75      80
Glu Ala Leu Arg Glu Asp Gly Ile Glu Ala Val Ala Ile Val Thr Pro
85      90      95
Asn His Val His Tyr Pro Ala Ala Lys Ala Phe Leu Glu Arg Gly Ile
100     105     110
His Val Ile Cys Asp Lys Pro Leu Thr Ser Asn Leu Glu Asp Ala Lys
115     120     125
Lys Leu Lys Asp Val Ala Asp Lys Ala Asp Ala Leu Phe Ile Leu Thr
130     135     140
His Asn Tyr Thr Gly Tyr Pro Met Val Arg His Ala Arg Glu Leu Val
145     150     155     160
Glu Ser Gly Ala Leu Gly Thr Ile Arg Leu Val Gln Met Glu Tyr Pro
165     170     175
Gln Asp Trp Leu Ala Glu Pro Ile Glu Gln Thr Gly Ala Lys Gln Ala
180     185     190
Val Trp Arg Thr Asp Pro Ala Gln Ser Gly Ala Gly Gly Ser Thr Gly
195     200     205
Asp Ile Gly Thr His Ala Tyr Asn Leu Gly Cys Phe Ile Ser Gly Leu
210     215     220
Glu Val Asp Glu Leu Ala Ala Asp Val His Thr Phe Val Glu Gly Arg
225     230     235     240
Arg Leu Asp Asp Asn Ala His Val Met Leu Arg Phe Lys Pro Lys Gly
245     250     255
Gly Lys Gln Pro Ala Lys Gly Leu Leu Trp Cys Ser Gln Val Ala Val
260     265     270
Gly His Glu Asn Gly Leu Lys Val Arg Val Tyr Gly Asp Lys Ala Gly
275     280     285
Ile Glu Trp Thr Gln Ala Asp Pro Asn Tyr Leu Trp Phe Thr Lys Leu
290     295     300
Gly Glu Leu Lys Gln Leu Ile Thr Arg Gly Gly Ala Gly Ala Gly Ala
305     310     315     320

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Ala Ala Ala Arg Val Thr Arg Ile Pro Ser Gly His Pro Glu Gly Tyr  
 325 330 335  
 Leu Glu Ala Phe Ala Thr Ile Tyr Thr Glu Ala Ala His Ala Ile Glu  
 340 345 350  
 Ala Arg Arg Thr Gly Ser Val Leu Asp Lys Ala Val Ile Tyr Pro Thr  
 355 360 365  
 Val Asp Asp Gly Val Lys Gly Val Ala Phe Val Thr Ala Cys Ile Glu  
 370 375 380  
 Ser Gly Lys Lys Asn Gly Val Trp Val Lys Leu  
 385 390 395

<210> 13  
 <211> 1059  
 <212> DNA  
 <213> *Xanthomonas campestris* pv. *campestris*

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 <222> (1).. (1059)  
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 cgc acc ttc cac gca ccg ctg atc gcc agc acg ccc gcc ctg cag ttg 96  
 Arg Thr Phe His Ala Pro Leu Ile Ala Ser Thr Pro Gly Leu Gln Leu  
 20 25 30  
 cac agc gtg tgc tgc tcc aag ccg cag caa ccg cag gcg gac ttc cgc 144  
 His Ser Val Val Ser Ser Lys Pro Gln Gln Pro Gln Ala Asp Phe Arg  
 35 40 45  
 gag gtg cgc gtg ctg ccc gac ctg gag gct gca ctg gcc gac ccg gcg 192  
 Glu Val Arg Val Leu Pro Asp Leu Glu Ala Ala Leu Ala Asp Pro Ala  
 50 55 60  
 ctg gat gcg gtg gtc atc gcc acg ccc aac cag acc cat gcg ccc atg 240  
 Leu Asp Ala Val Val Ile Ala Thr Pro Asn Gln Thr His Ala Pro Met  
 65 70 75 80  
 gcg ctg cag gca ctg gcg gcc gcc aag cac gtg ctg gtg gat aaa ccc 288  
 Ala Leu Gln Ala Leu Ala Ala Gly Lys His Val Leu Val Asp Lys Pro  
 85 90 95  
 ttc gcc ctg gat gcc gca cag gct cgc acc gtg gtg gac gcc gcc gca 336  
 Phe Ala Leu Asp Ala Ala Gln Ala Arg Thr Val Val Asp Ala Ala Ala  
 100 105 110  
 gag gcc gcc aag atc gtc agc gtg ttc cag aac cgc cgt tgg gat gcg 384  
 Glu Ala Gly Lys Ile Val Ser Val Phe Gln Asn Arg Arg Trp Asp Ala  
 115 120 125  
 gac ttc ctc acc gtg ccg cgc ttg atc gaa gac gcc caa ctg gcc gag 432

Asp Phe Leu Thr Val Arg Arg Leu Ile Glu Asp Gly Gln Leu Gly Glu	
130 135 140	
gtg gtg gag ttc cat tgc cac ttc gac cgg tat cgc ccg cag gtg cgc	480
Val Val Glu Phe His Ser His Phe Asp Arg Tyr Arg Pro Gln Val Arg	
145 150 155 160	
gac cgc tgg cgc gaa agc gat atc ccc ggc gcc ggg ctg tgg tac gac	528
Asp Arg Trp Arg Glu Ser Asp Ile Pro Gly Ala Gly Leu Trp Tyr Asp	
165 170 175	
ctg ggg ccg cat ctg ctg gac cag gcg ttg cag ttg ttc ggc atg ccg	576
Leu Gly Pro His Leu Leu Asp Gln Ala Leu Gln Leu Phe Gly Met Pro	
180 185 190	
cag gcg atc agc gca gac ctg cag cgc cag cgc acc cag gcg cgc agc	624
Gln Ala Ile Ser Ala Asp Leu Gln Arg Gln Arg Thr Gln Ala Arg Ser	
195 200 205	
gac gat tac ttc aac gtg gtg ctg cgc tat ccc cgc ttg cgg gtg atc	672
Asp Asp Tyr Phe Asn Val Val Leu Arg Tyr Pro Arg Leu Arg Val Ile	
210 215 220	
ctg cac gcc ggc tgc ctg gtg gcc gac ggc agc ctg cgc ttc gcc gtg	720
Leu His Ala Gly Ser Leu Val Ala Asp Gly Ser Leu Arg Phe Ala Val	
225 230 235 240	
cac ggc acg cgc ggc agc tat ctc aag cat ggc gcc gat acg cag gaa	768
His Gly Thr Arg Gly Ser Tyr Leu Lys His Gly Ala Asp Thr Gln Glu	
245 250 255	
gac cag ttg cgt gcc ggc cgc cgg ccc ggc acc gcc ggc tgg ggc atg	816
Asp Gln Leu Arg Ala Gly Arg Arg Pro Gly Thr Ala Gly Trp Gly Met	
260 265 270	
gac cca ttg ccc ggc acg ctc acc cgc gtg gac gac gaa ggc cgt gtg	864
Asp Pro Leu Pro Gly Thr Leu Thr Arg Val Asp Asp Glu Gly Arg Val	
275 280 285	
cac acg cat cag ccc gat ggc gta ccc ggc gac tac cgc cat tgc tat	912
His Thr His Gln Pro Asp Gly Val Pro Gly Asp Tyr Arg His Cys Tyr	
290 295 300	
gcg gcc ttc cgc gac gca atg gcc ggc acc gca ccg cca ccg gtc agt	960
Ala Ala Phe Arg Asp Ala Met Ala Gly Thr Ala Pro Pro Pro Val Ser	
305 310 315 320	
gct gcc gac gcg gtg cgg ctg atg gag ctg ctg gag ctg gcg caa cgc	1008
Ala Ala Asp Ala Val Arg Leu Met Glu Leu Leu Glu Leu Ala Gln Arg	
325 330 335	
ggt gct gcg ctg ggc cag gtg ctc tgg ctg gaa ggc aac agc agc gac	1056
Gly Ala Ala Leu Gly Gln Val Leu Trp Leu Glu Gly Asn Ser Ser Asp	
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tga	1059

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 <211> 352  
 <212> PRT

<213> *Xanthomonas campestris* pv. *campestris*

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 His Ser Val Val Ser Ser Lys Pro Gln Gln Pro Gln Ala Asp Phe Arg  
 35 40 45  
 Glu Val Arg Val Leu Pro Asp Leu Glu Ala Ala Leu Ala Asp Pro Ala  
 50 55 60  
 Leu Asp Ala Val Val Ile Ala Thr Pro Asn Gln Thr His Ala Pro Met  
 65 70 75 80  
 Ala Leu Gln Ala Leu Ala Ala Gly Lys His Val Leu Val Asp Lys Pro  
 85 90 95  
 Phe Ala Leu Asp Ala Ala Gln Ala Arg Thr Val Val Asp Ala Ala Ala  
 100 105 110  
 Glu Ala Gly Lys Ile Val Ser Val Phe Gln Asn Arg Arg Trp Asp Ala  
 115 120 125  
 Asp Phe Leu Thr Val Arg Arg Leu Ile Glu Asp Gly Gln Leu Gly Glu  
 130 135 140  
 Val Val Glu Phe His Ser His Phe Asp Arg Tyr Arg Pro Gln Val Arg  
 145 150 155 160  
 Asp Arg Trp Arg Glu Ser Asp Ile Pro Gly Ala Gly Leu Trp Tyr Asp  
 165 170 175  
 Leu Gly Pro His Leu Leu Asp Gln Ala Leu Gln Leu Phe Gly Met Pro  
 180 185 190  
 Gln Ala Ile Ser Ala Asp Leu Gln Arg Gln Arg Thr Gln Ala Arg Ser  
 195 200 205  
 Asp Asp Tyr Phe Asn Val Val Leu Arg Tyr Pro Arg Leu Arg Val Ile  
 210 215 220  
 Leu His Ala Gly Ser Leu Val Ala Asp Gly Ser Leu Arg Phe Ala Val  
 225 230 235 240  
 His Gly Thr Arg Gly Ser Tyr Leu Lys His Gly Ala Asp Thr Gln Glu  
 245 250 255  
 Asp Gln Leu Arg Ala Gly Arg Arg Pro Gly Thr Ala Gly Trp Gly Met  
 260 265 270  
 Asp Pro Leu Pro Gly Thr Leu Thr Arg Val Asp Asp Glu Gly Arg Val  
 275 280 285  
 His Thr His Gln Pro Asp Gly Val Pro Gly Asp Tyr Arg His Cys Tyr  
 290 295 300  
 Ala Ala Phe Arg Asp Ala Met Ala Gly Thr Ala Pro Pro Pro Val Ser  
 305 310 315 320  
 Ala Ala Asp Ala Val Arg Leu Met Glu Leu Leu Glu Leu Ala Gln Arg  
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31

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32

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<220>  
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35

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39



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 ggg cgc acc cac gcc ttt ggc tat tca acc gcg tcc cgt gtg ttt gat 96  
 Gly Arg Thr His Ala Phe Gly Tyr Ser Thr Ala Ser Arg Val Phe Asp  
 20 25 30  
 ctt ccg ttt cag ccg gag ctg acg tgc ctg gct gat att tcc gat gaa 144  
 Leu Pro Phe Gln Pro Glu Leu Thr Cys Leu Ala Asp Ile Ser Asp Glu  
 35 40 45  
 gct gca gcg aag gcg gcg gat gct ctg gga ttt gcc cgt tcc acc agt 192  
 Ala Ala Ala Lys Ala Ala Asp Ala Leu Gly Phe Ala Arg Ser Thr Ser  
 50 55 60  
 gac tgg cgt acg ctc gtc aac gat cct gaa att gat gtg gtg aat atc 240  
 Asp Trp Arg Thr Leu Val Asn Asp Pro Glu Ile Asp Val Val Asn Ile  
 65 70 75 80  
 acg gcg cct aat gcc ttt cat aaa gaa atg gcg tta gca gcg att gct 288  
 Thr Ala Pro Asn Ala Phe His Lys Glu Met Ala Leu Ala Ala Ile Ala  
 85 90 95  
 gcg ggc aag cat gtc tat tgt gaa aag ccc ctt gcg cca ctt gca gcc 336  
 Ala Gly Lys His Val Tyr Cys Glu Lys Pro Leu Ala Pro Leu Ala Ala  
 100 105 110  
 gat gct cgc gaa atg gca gaa gcg gct gag gca aag ggc gta aaa aca 384  
 Asp Ala Arg Glu Met Ala Glu Ala Ala Glu Ala Lys Gly Val Lys Thr  
 115 120 125  
 cag gtt ggc ttc aac tac ctg tgc aac ccc atg ctg gca ctg gcc cga 432  
 Gln Val Gly Phe Asn Tyr Leu Cys Asn Pro Met Leu Ala Leu Ala Arg  
 130 135 140  
 gat atg att gca gca ggg gag ctg ggg gaa atc aga ggg tac cgt ggc 480  
 Asp Met Ile Ala Ala Gly Glu Leu Gly Glu Ile Arg Gly Tyr Arg Gly  
 145 150 155 160  
 ctg cat gcg gaa gat tat atg gcg gac gcc tcg tct ccc ttt acg ttc 528  
 Leu His Ala Glu Asp Tyr Met Ala Asp Ala Ser Ser Pro Phe Thr Phe  
 165 170 175  
 cgt ctt gac cca gcg gga ggc ggc gca ctt gct gat att ggg agt cac 576  
 Arg Leu Asp Pro Ala Gly Gly Gly Ala Leu Ala Asp Ile Gly Ser His  
 180 185 190

gcc ctt gca acg gct gaa ttt ctt atg ggg cct gcc gca ggc gct atc 624  
 Ala Leu Ala Thr Ala Glu Phe Leu Met Gly Pro Ala Ala Gly Ala Ile  
 195 200 205  
 acg cag gtg atg ggg gat tgt gtg acg gtc atc aag acg cgg ccg gat 672  
 Thr Gln Val Met Gly Asp Cys Val Thr Val Ile Lys Thr Arg Pro Asp  
 210 215 220  
 ggt aag ggg gga acg cgg gct gta gaa gtg gac gat att ggc cgc gcg 720  
 Gly Lys Gly Gly Thr Arg Ala Val Glu Val Asp Asp Ile Gly Arg Ala  
 225 230 235 240  
 ctt ctg cgc ttt gag aat ggg cgc acg gga tcg gtt gag gga aac tgg 768  
 Leu Leu Arg Phe Glu Asn Gly Ala Thr Gly Ser Val Glu Gly Asn Trp  
 245 250 255  
 att gct acc ggc cgc acc atg cag cat gac ttt gag gta tac ggc aca 816  
 Ile Ala Thr Gly Arg Thr Met Gln His Asp Phe Glu Val Tyr Gly Thr  
 260 265 270  
 aaa ggt gca ctt gcc ttt act cag caa cga ttt aac gag ttg cat ttc 864  
 Lys Gly Ala Leu Ala Phe Thr Gln Gln Arg Phe Asn Glu Leu His Phe  
 275 280 285  
 ttc tca agc acc gat gca cgc ggc cgc aaa ggg ttc cgg cgt att gaa 912  
 Phe Ser Ser Thr Asp Ala Arg Gly Arg Lys Gly Phe Arg Arg Ile Glu  
 290 295 300  
 gcg gga cca gag cat gcg ccc tat ggc ctg ttc tgc gtg gca ccg ggg 960  
 Ala Gly Pro Glu His Ala Pro Tyr Gly Leu Phe Cys Val Ala Pro Gly  
 305 310 315 320  
 cac cag ctg ggt ttt aat gac ctc aag gcg ata gaa gtt gca cgg tat 1008  
 His Gln Leu Gly Phe Asn Asp Leu Lys Ala Ile Glu Val Ala Arg Tyr  
 325 330 335  
 ctg gag gcg ctg gct ggc cat cac cct gaa ccc ttc aat ttc cgg gcg 1056  
 Leu Glu Ala Leu Ala Gly His His Pro Glu Pro Phe Asn Phe Arg Ala  
 340 345 350  
 ggt ctg cgt atc cag aca ctg gtg gaa act att cac gct tca agc aag 1104  
 Gly Leu Arg Ile Gln Thr Leu Val Glu Thr Ile His Ala Ser Ser Lys  
 355 360 365  
 tcg gct gcc tgg cgg gat gtg ccg acg gac aaa gtg aag ctt cag gcg 1152  
 Ser Ala Ala Trp Arg Asp Val Pro Thr Asp Lys Val Lys Leu Gln Ala  
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 aaa tcc cga cag cat gag aag gca taa 1179  
 Lys Ser Arg Gln His Glu Lys Ala  
 385 390

<210> 28

<211> 392

<212> PRT

<213> Acetobacter sp.

<400> 28

Met Thr Lys Arg Lys Leu Arg Ile Gly Leu Ile Gly Ser Gly Phe Met

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		20		25		30
Leu	Pro	Phe	Gln	Pro	Glu	Glu
		35		40		45
Ala	Ala	Ala	Lys	Ala	Ala	Ser
		50		55		60
Asp	Trp	Arg	Thr	Leu	Val	Ile
65			70		75	80
Thr	Ala	Pro	Asn	Ala	Phe	Ala
			85		90	95
Ala	Gly	Lys	His	Val	Tyr	Ala
		100		105		110
Asp	Ala	Arg	Glu	Met	Ala	Thr
		115		120		125
Gln	Val	Gly	Phe	Asn	Tyr	Arg
		130		135		140
Asp	Met	Ile	Ala	Ala	Gly	Gly
145			150		155	160
Leu	His	Ala	Glu	Asp	Tyr	Thr
			165		170	175
Arg	Leu	Asp	Pro	Ala	Gly	His
		180		185		190
Ala	Leu	Ala	Thr	Ala	Glu	Ile
		195		200		205
Thr	Gln	Val	Met	Gly	Asp	Asp
		210		215		220
Gly	Lys	Gly	Gly	Thr	Arg	Ala
225			230		235	240
Leu	Leu	Arg	Phe	Glu	Asn	Trp
			245		250	255
Ile	Ala	Thr	Gly	Arg	Thr	Thr
		260		265		270
Lys	Gly	Ala	Leu	Ala	Phe	Phe
		275		280		285
Phe	Ser	Ser	Thr	Asp	Ala	Glu
		290		295		300
Ala	Gly	Pro	Glu	His	Ala	Gly
305			310		315	320
His	Gln	Leu	Gly	Phe	Asn	Tyr
			325		330	335
Leu	Glu	Ala	Leu	Ala	Gly	Ala
		340		345		350
Gly	Leu	Arg	Ile	Gln	Thr	Lys
		355		360		365
Ser	Ala	Ala	Trp	Arg	Asp	Ala
		370		375		380
Lys	Ser	Arg	Gln	His	Glu	Ala

385

390

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<220>  
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 <223> n=inosine

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32

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32

<210> 31  
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<400> 31  
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26

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19

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<400> 33  
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25

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25

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21

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26

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<400> 37  
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31